

FIG. 1

BLASTP - query = 147\_TR1; Hit = swiss|O15393|TMS2\_HUMAN

This hit is scoring at : 3e-66 (expectation value)

Alignment length (overlap) : 370

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 36 CDGVVDCKLKSDELGCVRFDWKSLKIIYSGSSHQWLPICSSNWNDSEKTCQQLGFES  
CDGV .C. .DE CVR. . . :L::YS.....W P:C...WN::Y....C::G:::  
H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPVCQDDWNNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST-----IQESLHRSE-CPSQRYISLQCSHCGLR---A  
. ::: . D :.S S:::N:: I...L:.S: C.S:::SL:C CG:. :  
NFYSSQGIVDD-SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPQVSLHFGTTHICGGTLIDAQWVLTAAHCFVVTREKVLEG---  
...RIVGG. A ...WPWQVSLH. ..H:CGG::I...W::TAAHC. EK L..  
RQSRIVGGESALPGAWPQVSLHVQNVHVCGGSIIITPEWIVTAAHCV----EKPLNNPWH

**TRYPSIN\_HIS**

WKVYAGTSNLHQLPEAAS--IAEIIINSNYTDEEDDYDIALMRLSKPLTLSG--EGICTP  
W...AG. . . : .A. ::::I :.NY.....: DIALM:L.KPLT... : :C.P  
WTAFAGILRQSFMYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPQHPLQPSHLASVNSYPGPKASADKTSPFLREVQVNLIDFKKCDYLVYDSYL  
. P LQP..L . :::: G.....KTS..L...:V LI: ::CN. .VYD::  
N-----PGMMLQPEQL-CWISGW-GATEEKGKTSEVLNAAKVLLIETQRCNSRYVDNLI

TPRMMCAGDLRGGRDSCQGDSSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPVGVTYTKVTEV  
TP.M:CAG L:G. DSCQGDSSGGPLV...NN W:L.G TSWG:GC... :PGVY .V. .  
TPAMICAGFLQGNVDSCQGDSSGGPLVTSNNNIWWLIGDTSWGSQCAKAYRPGVYGNVMVF

**TRYPSIN\_SER**

LPWIYSKMEA 389  
..WIY.:M:A  
TDWIYRQMK 490

BLOCKS

FIG. 2

Prosite search results

PS00134	187->193	TRYPSIN_HIS	PDOC00124
PS00135	334->346	TRYPSIN_SER	PDOC00124

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FIG. 3

## BLOCKS search results

AC# Score	Description	Strength	
BL00495N AA#	Apple domain proteins. 325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)	1945	1582
BL01253G AA#	Type I fibronectin domain proteins. 332 rDsCQGDSGGPLVC (SEQ ID NO:16)	1641	1548
BL00134A AA#	Serine proteases, trypsin family, histidine p 1500 175 CGGTLIDaQWVLTAHC (SEQ ID NO:17)	1524	
BL00021D AA#	Kringle domain proteins. 341 GPLVCEQNNRWYLaGVTSWGtGCGQRNKPVGVTevLPWI (SEQ ID NO:18)	1556	1510
BL01253H AA#	Type I fibronectin domain proteins. 351 wYLaGvtSWGtGCGQRNKPVGVTevLpWIysk (SEQ ID NO:19)	1765	1508
BL00021B AA#	Kringle domain proteins. 175 CGGTLIDaQWVLTAHCF (SEQ ID NO:120)	1547	1507
BL00495O AA#	Apple domain proteins. 360 GtGCGQRnkPGVYTKVtEvlpWIysKmeA (SEQ ID NO:121)	1756	1383
BL00134B AA#	Serine proteases, trypsin family, histidine p 1289 333 DSCQGDGGPLVCEqNNRWYLAGV (SEQ ID NO:122)	1289	1299
BL01209 AA#	LDL-receptor class A (LDLRA) domain proteins. 35 CDGVVDCKlKSDE (SEQ ID NO:123)	1413	1274
BL01253F AA#	Type I fibronectin domain proteins. 288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:124)	1693	1270
BL00495L AA#	Apple domain proteins. 209 tSnlhqlpeaaSIaEIIInsNYtdeEddYDIALmrLskP (SEQ ID NO:125)	1947	1263
BL00134C AA#	Serine proteases, trypsin family, histidine p 1245 369 PGVYTKVTEVLPWI (SEQ ID NO:126)	1245	1254
BL01253D AA#	Type I fibronectin domain proteins. 175 CGGtLIIdaqWVLTA (SEQ ID NO:127)	1398	1217

FIG. 4

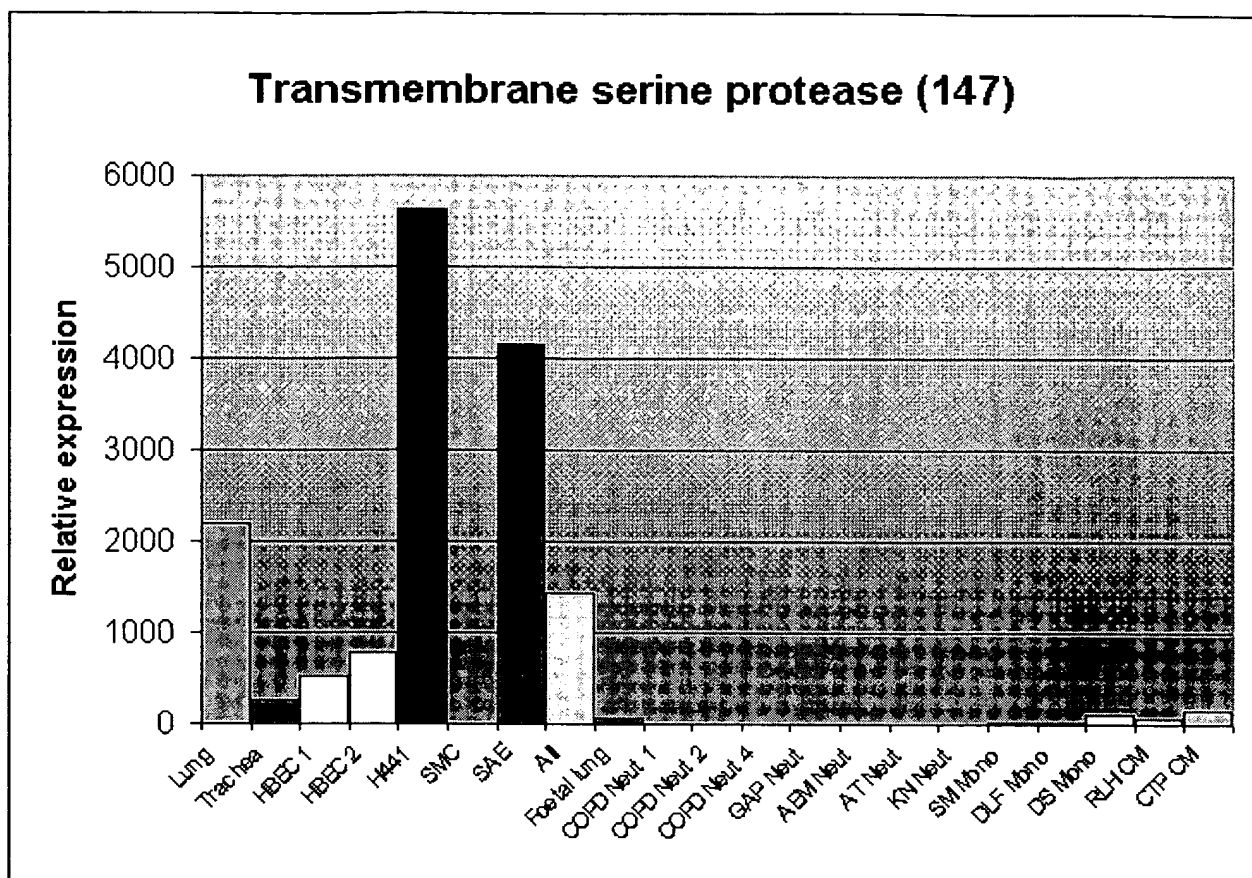
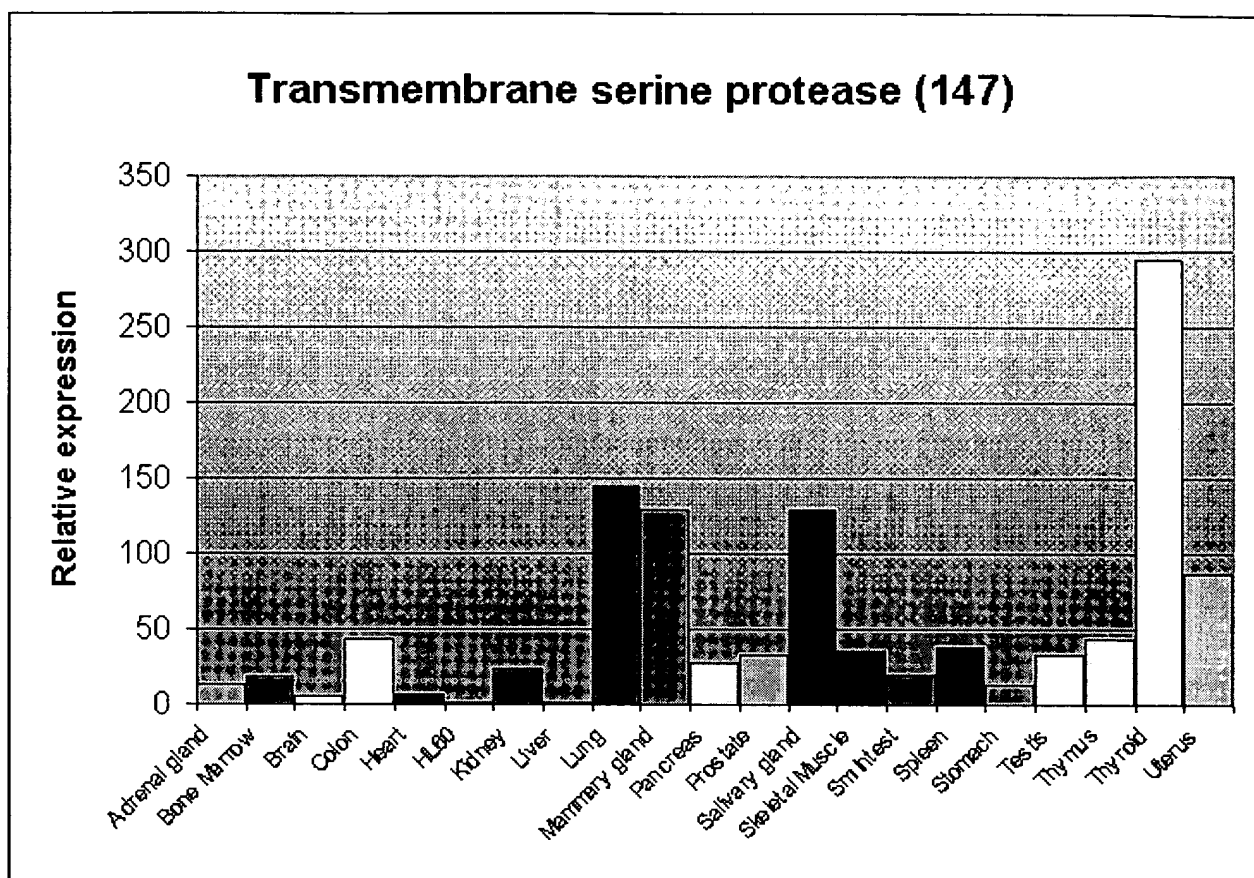
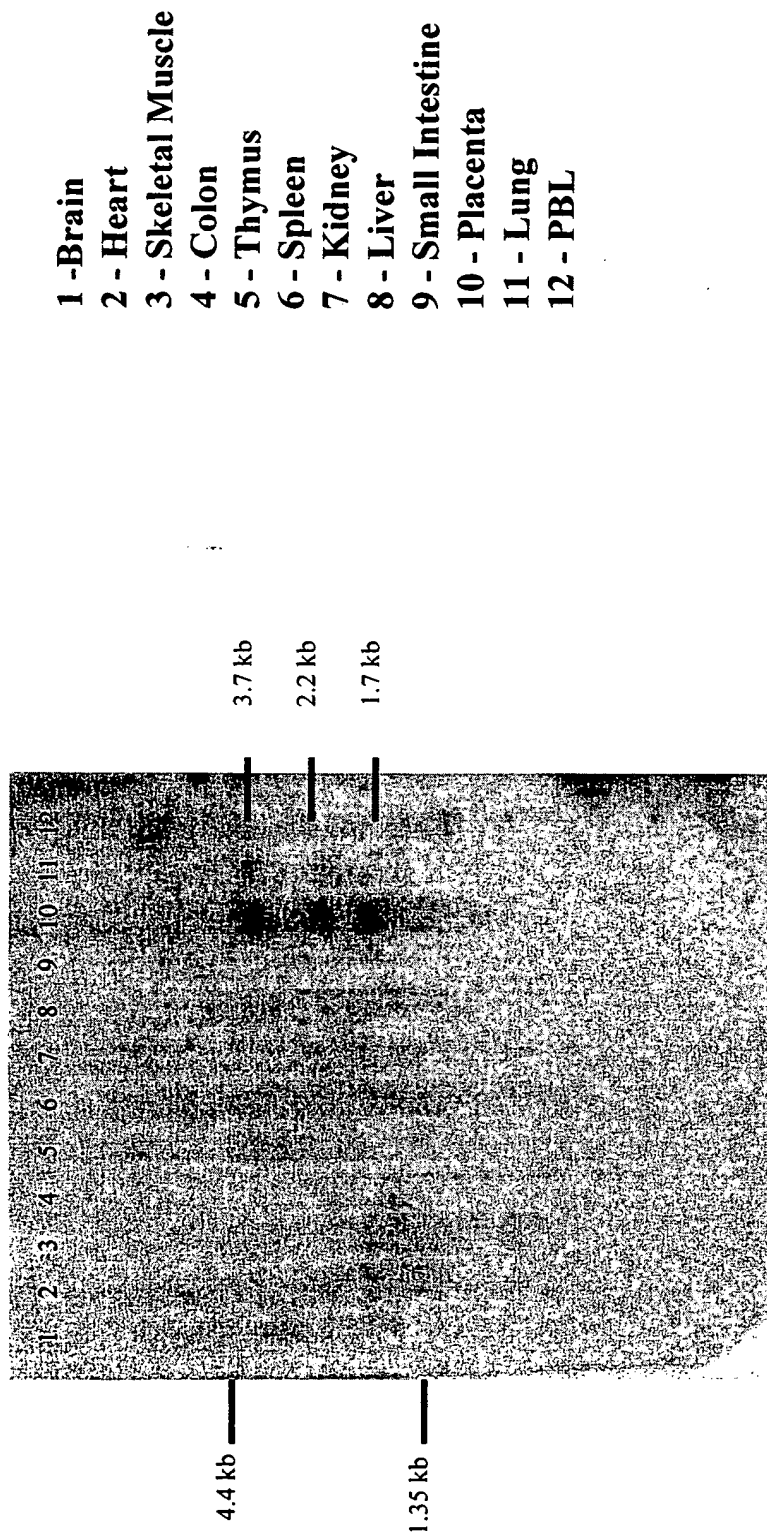


FIG. 5



# LBRI - 147 - Transmembrane serine protease



16 hour exposure - Maximum Intensity 2,000

LBRI 147

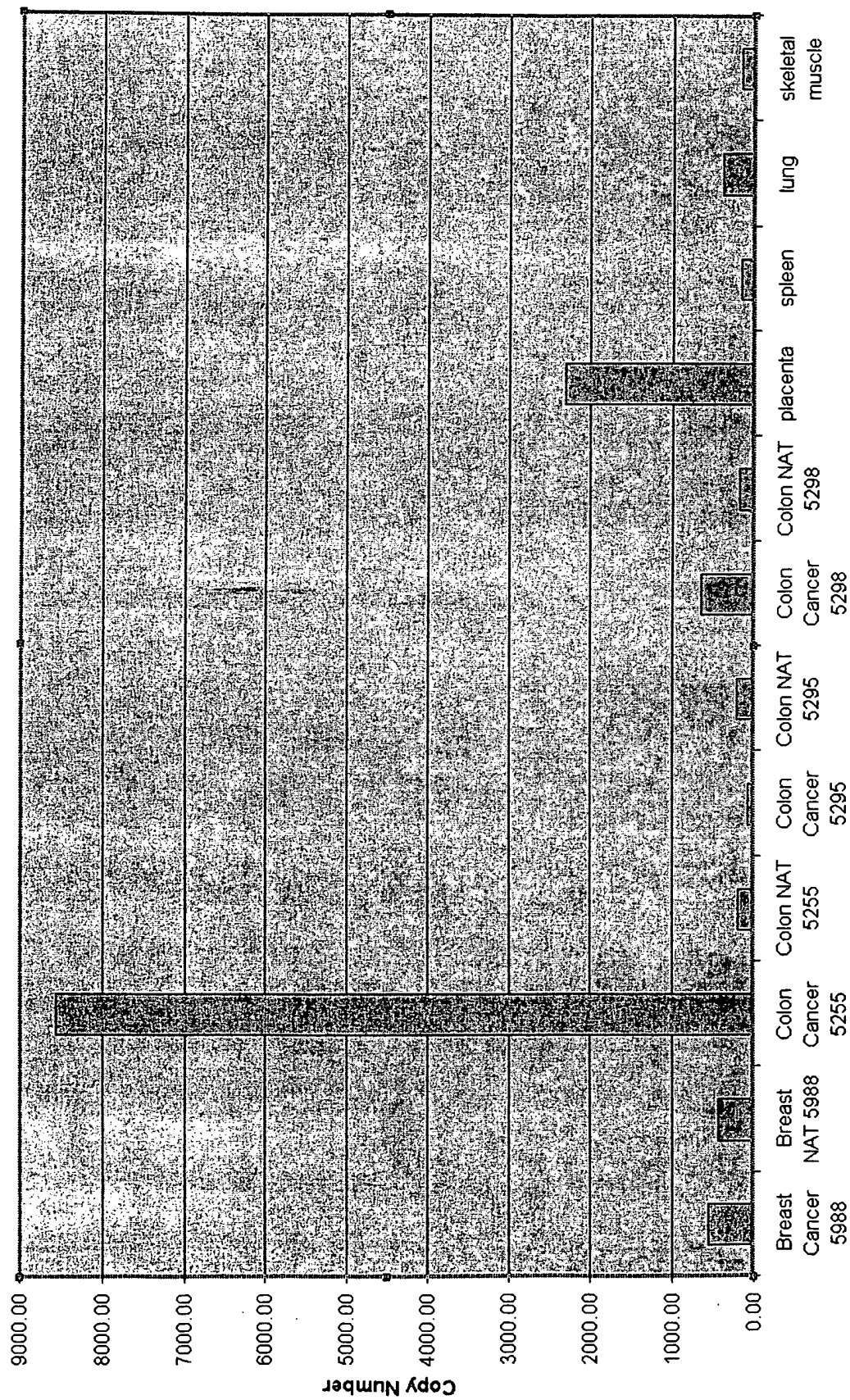
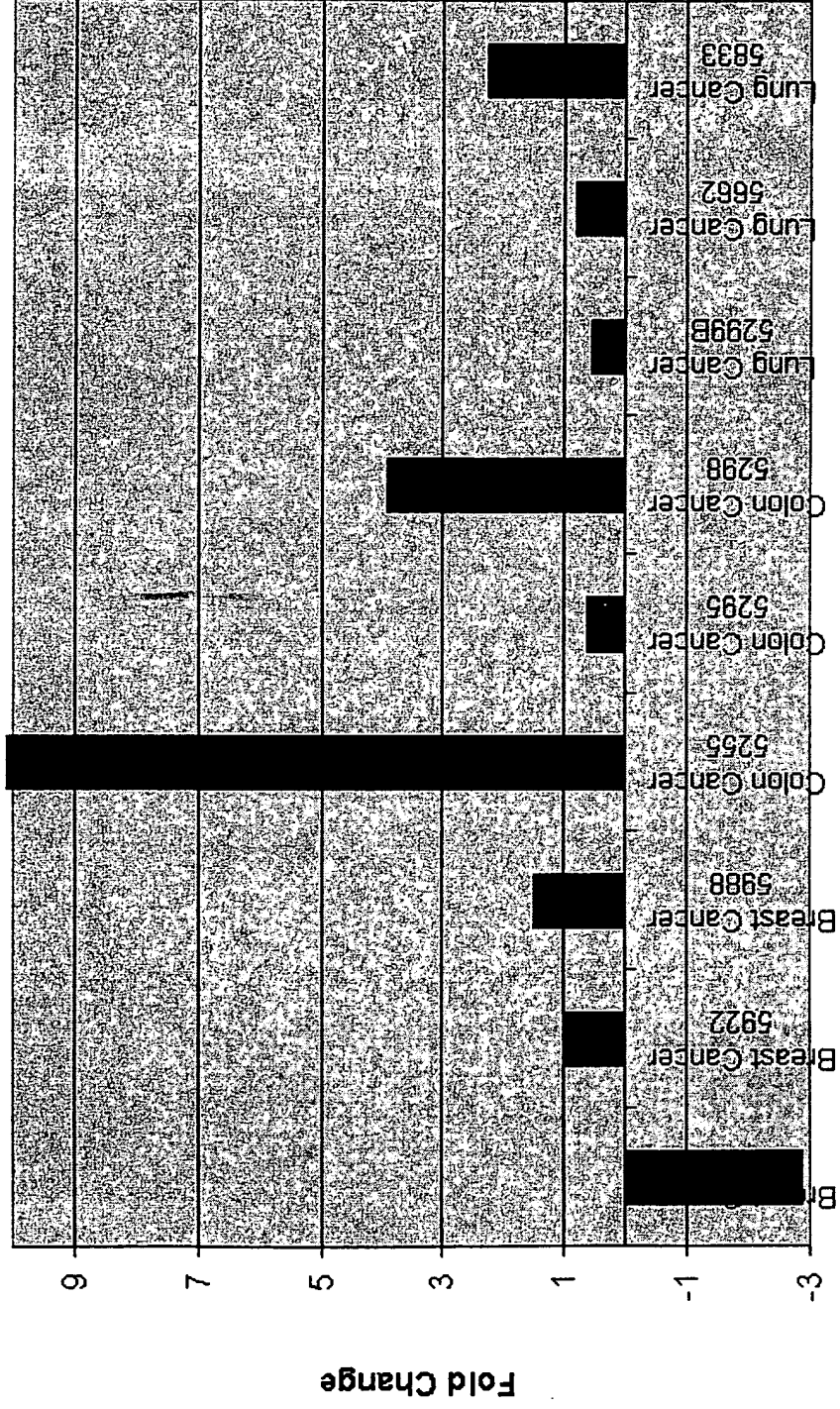


FIG. 7

LBRI 147 - Fold change

74.





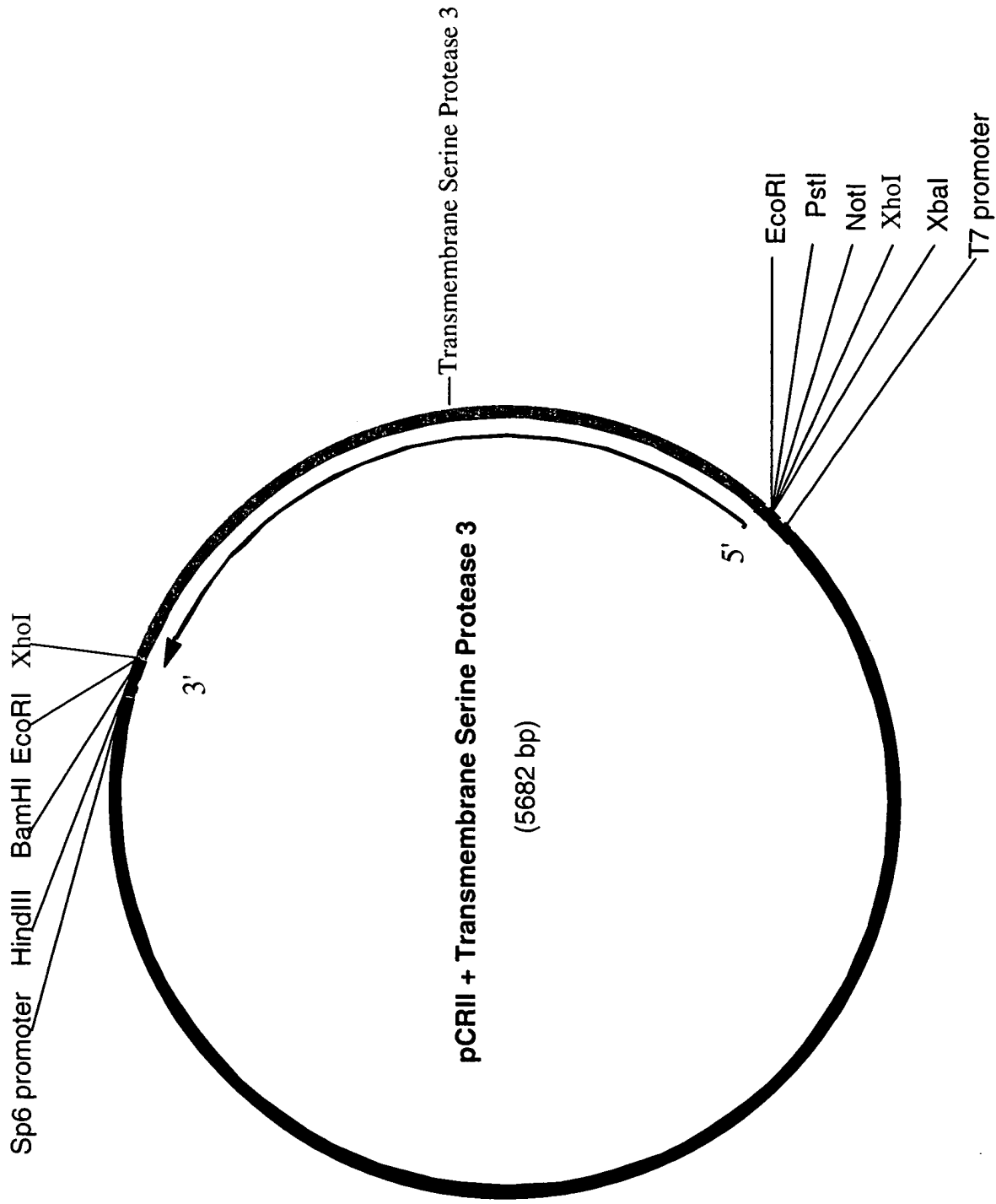


Fig. 9